REMARKS

Status of the Claims.

In response to the Office Action dated February 25, 2004, Applicants filed an Amendment in the instant application on August 25, 2004. On November 9, 2004, Examiner Leffers informed Applicants' attorney by telephone that the Amendment was not fully responsive because the dependency of claim 111 had been changed without indicating that the claim had been amended as required under 37 CFR § 1.121 and it was not clear whether the rejection of claim 36 under 35 USC § 112 had been addressed. The Examiner stated that a Notice of Non-Responsive Amendment would be subsequently mailed. On November 22, 2004, Applicants received a Notice of Non-Responsive Amendment, which requesting that a new Amendment be filed. The instant Amendment addresses the Examiner's concerns. Applicants understand from the Examiner that the Amendment filed on August 25, 2004 has not been entered. The instant Amendment is thus responsive to the Office Action mailed on February 24, 2004 and the claims pending as of that date.

Applicants note that claims 4 and 110 were substantively allowed in the Office Action dated February 25, 2004 and thank the Examiner for substantive allowance of these claims.

Claims 1, 3-4, 7-8, 10-11, 14-18, 21-23, 26-28, 31, 33, 35-36, 44, 46-48, 62-66, 74-79, 93-94, 106-107, 113-116, 118-126 are pending with the entry of this amendment. Claims 2, 5-6, 9, 12-13, 19-20, 24-25, 29-30, 32, 34, 37-43, 45, 49-61 , 67-73, 80-92, 95-105, 108-112, and 117 have been canceled without prejudice to subsequent renewal, including in a divisional or continuation application. Claims 1, 3, 7-8, 10, 21-23, 26-28, 31, 33, 35-36, 44, 46, 62, 65, 74, 93, 106, 113-116, and 118-119 are amended herein without prejudice to subsequent renewal of any subject matter canceled from any claim herein. All of the amendments to the pending claims introduce no new matter and are fully supported by the specification as filed. Applicants reserve the right to pursue and/or renew subject matter canceled from any claim herein without prejudice, including in a divisional or continuation application.

New claims 120-126 have been added. Each of these new claims is fully supported by the specification as filed and includes no new matter. New claim 120, which is dependent on claim 7, further specifies that the polynucleotide sequence promotes expression of a nucleic acid encoding a polypeptide to which the sequence is operably linked at a level greater than the level of expression when the poly-peptide-encoding nucleic acid is linked to the human CMV promoter shown in SEQ ID NO:10 or SEQ ID NO:20. Support for this amendment is provided throughout the

specification, including at, *e.g.*, original claim 8. New claims 121 and 122 specify a vector comprising at least one nucleic acid of claim 4 or 7, respectively. Support for this amendment is provided at, *e.g.*, original claim 62.

New claim 123, which depends from claim 122, further specifies that the polynucleotide sequence promotes expression of a nucleic acid encoding a polypeptide to which the polynucleotide sequence is operably linked at a level greater than the level of expression of the polypeptide-encoding nucleic acid when the polypeptide-encoding nucleic acid is operably linked to the human CMV promoter sequence shown in SEQ ID NO:19 or SEQ ID NO:20. Support for this amendment is provided at, *e.g.*, original claim 8.

New claim 124, which depends from claim 27, further indicates that the polynucleotide sequence has at least 99.5% sequence identity to a nucleotide sequence which comprises the sequence of SEQ ID NO:8 with a deletion of one or more nucleotide residues in a region corresponding to nucleotide residue positions 684-735 of the consensus sequence shown in SEQ ID NO:21, or to a complementary sequence thereof. Support for this amendment is provided throughout the specification, including at, *e.g.*, original claims 1, 3, 7, and 27-28, 37; page 11, lines 1-5; page 19, lines 15-16; and page 10, lines 9-11. The specification specifically provides for chimeric CMV promoter/enhancer homologue nucleic acids having at least 99.5% sequence identity to the sequence of SEQ ID NO:8 or to fragments thereof. *See, e.g.*, page 11, lines 1-5. Particular fragments of SEQ ID NO:8 are described. A fragment of SEQ ID NO:8 that lacks one or more nucleotide residues in a region corresponding to residue positions 684-735 of the consensus sequence shown in SEQ ID NO:21 is specifically described. *See, e.g.*, original claim 27.

New claim 125, which depends from claim 35, further recites that the polynucleotide sequence has at least 99.5% sequence identity to a nucleotide sequence which comprises the sequence of SEQ ID NO:8 with a deletion of one or more nucleotide residues in a region corresponding to residue positions 319-512 of the consensus sequence shown in SEQ ID NO:21. Support for this amendment is provided at, *e.g.*, original claims 1, 3, 7, and 35-37; page 11, lines 1-5; page 19, lines 15-16; and page 10, lines 9-11. The specification plainly provides for chimeric CMV promoter/enhancer homologue nucleic acids having at least 99.5% sequence identity to fragments of SEQ ID NO:8. *See, e.g.*, page 11, lines 1-5. A fragment of SEQ ID NO:8 which lacks one or more nucleotide residues in a region corresponding to residue positions 319-512 of the consensus sequence shown in SEQ ID NO:21 is specifically described. *See, e.g.*, original claim 35.

New claim 126, which depends from claim 113, further specifies that the promoter comprises a polynucleotide sequence having at least 99.5% sequence identity to the entire length of the sequence of SEQ ID NO:8. Support for this amendment is provided in the specification, including at, *e.g.*, original claims 1, 3, 7, and 62; page 11, lines 1-5.

Claims 10 and 12 have been canceled by entry of this Amendment. Consequently, claims 44, 62, 65, and 74 have been amended to delete reference to these canceled claims. Claim 31 has been rewritten as an independent claim and claim 33 has been amended to depend from claim 31. Claim 46 has been amended to incorporate the limitations of claim 45, and thus claim 45 has been canceled. Claims 114-116 have been amended to correct an inadvertent error in claim dependency; each of these claims now depends properly from claim 113. Claim 118 has been amended to depend from claim 113. Claim 119 has been amended to correct an inadvertent error in claim dependency; claim 119 now depends properly from claim 118.

Rejections Under 35 USC § 112, First Paragraph.

Claims 3, 8, 14-18, and 105 were rejected under 35 USC § 112, first paragraph, as allegedly failing to comply with the written description requirement. The Examiner takes the position that the "rejected claims encompass a large genus of polynucleotide sequences that must retain the recited structural identity to SEQ ID NO:8 as well as retaining the recited functional activity relative to that of the reference CMV promoters." Office Action, page 3, 3rd full para. The Examiner finds that "the skilled artisan would not have been able to envision a sufficient number of specific embodiments embraced by the claims to describe the broadly claimed genus of nucleic acids having the recited functional activity" and thus "the skilled artisan would reasonably have concluded applicants were not in possession of the claimed invention." *Id.* at page 5, 1st para.

The rejection of claim 105 has been mooted by its cancellation. The rejection of claims 3, 8, and 14-18 is respectfully traversed as follows.

The Federal Circuit has discussed the written description requirement in reference to inventions involving a chemical genus. *See Univ. of California v. Eli Lilly and Co.*, 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In *Lilly*, the Court explained:

> In claims involving chemical materials, generic formulae usually indicate with specificity what the generic claims encompass. One skilled in the art can distinguish such a formula from others and can identify many of the species that the claims encompass. Accordingly, such a formula is normally an adequate description of the claimed genus . . . However, a generic statement

> such as "vertebrate insulin cDNA" or "mammalian insulin cDNA," without more, is not an adequate written description of the genus because it does not distinguish the claimed genus from others, except by function. It does not specifically define any of the genes that fall within its definition. *It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is.*

Id.

The *Lilly* Court further explained that "[a] written description of an invention involving a chemical genus, like a description of a chemical species, 'requires a precise definition, such as by structure, formula, [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." *Id.* at 1567, 43 USPQ2d at 1405. The Court noted that "[a] description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." *Id.* at 1568, 43 USPQ2d at 1406.

The Federal Circuit further clarified the written description requirement in the context of DNA-related inventions in *Enzo Biochem, Inc. v. Gen-Probe Inc.*, 296 F.3d 1316, 63 USPQ2d 1609 (Fed. Cir. 2002). In *Enzo*, the Court explained that "the written description requirement can be met by 'showing that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics . . . i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics.'" *Id.* at 1324, 63 USPQ2d at 1613 (citing the USPTO's Written Description Guidelines, 66 Fed. Reg. 1099 *et seq.*, 1106). Notably, the *Enzo* Court adopted the standard for determining compliance with written description set forth in the USPTO's Written Description Examination Guidelines, which apply to protein sequences and DNA sequences.

Recently, the Federal Circuit reiterated the standard articulated in *Enzo*, stating that the written description requirement may be satisfied if in the knowledge of the art the disclosed function is sufficiently correlated to a particular structure. *Moba, B.V. v. Diamond Automation, Inc.*, 325 F.3d 1306, 1320, 66 USPQ2d 1429, 1438-39 (Fed. Cir. 2003), *rehearing denied* (Apr. 25, 2003);

p*etition for cert. filed*, 72 U.S.L.W. 3106 (U.S. Jul. 24, 2003) (No. 03-124). *Moba* stressed again that "[t]he test for compliance with § 112 has always required sufficient information in the original disclosure to show that the inventor possessed the invention at the time of the original filing . . . '[t]he written description requirement does not require the applicant to describe exactly the subject matter claimed, [instead] the description must clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed. . . .'" *Moba*, 352 F.3d at 1320-1321, 66 USPQ2d at 1439, quoting *Union Oil Co. of Cal. V. Atlantic Richfield Co.*, 208 F.3d 989,997, 54 USPQ2d 1227, 1232 (Fed. Cir. 2000).

Applicants respectfully submit that all of the rejected claims meet the written description requirement as elucidated by these Federal Circuit decisions as well as the USPTO's Written Description Guidelines. The Examiner's argument that written description requirement is not met because there is a lack of means to envision *a priori* which particular sequences will meet the functional limitations of the claims and thus one of skill would not have been able to envision a sufficient number of specific embodiments embraced by the claims is misplaced. Predictability is not the legal standard or test for such a rejection. The issue is whether Applicants have presented sufficiently detailed and relevant identifying characteristics, such as structure, function, chemical properties, etc., or a combination thereof, such that one of skill would understand, based upon reading the specification, that Applicants were in possession of the claimed nucleic acids at the time of filing. Here, the written description requirement is plainly met because Applicants describe specific chemical structures having a particular function, disclose a specific correlation between the claimed structures and the asserted function, and provide a specific description of the assays one can use to test whether a particular sequence has the asserted function. Based on Applicants' disclosure, one skilled in the art would certainly have recognized that Applicants were in possession of the claimed nucleic acids.

Notably, each of claims 3, 8, and 14-18 ultimately depends from independent claim 1, which the Examiner has found meets the written description requirements. As amended, claim 1 is directed to an isolated or recombinant nucleic acid comprising a polynucleotide sequence that has at least 99% sequence identity to the entire length of the polynucleotide sequence of SEQ ID NO:8 (or the complementary sequence thereof), wherein the polynucleotide sequence promotes expression of a nucleic acid encoding a polypeptide to which the polynucleotide sequence is operably linked.

Dependent claims 3, 8, and 14-18 simply specify more particularly the function of a specific nucleic acid (e.g., the polynucleotide sequence promotes expression of the polypeptide-encoding nucleic acid at a level that is equal to or greater than the level of expression of the polypeptide-encoding nucleic acid when the polypeptide-encoding nucleic acid is operably linked to the human CMV promoter polynucleotide sequence shown in SEQ ID NO:19 or SEQ ID NO:20). These dependent claims also satisfy the written description requirement outlined by the Federal Circuit and the USPTO's Written Description Guidelines. The specification plainly describes methods for determining whether a nucleic acid that is 99% identical to SEQ ID NO:8 promotes expression of the polypeptide-encoding nucleic acid at a level that is equal to or greater than the expression level when the polypeptide-encoding nucleic acid is operably linked to the human Towne or AD169 CMV promoter. The specification provides clear guidance and examples of such functional assays. Based on the specification's teachings, a skilled artisan would readily have been able to determine whether a nucleic acid sequence that is at least 99% identical to SEQ ID NO:8 has the required function. Given that the specification describes detailed common structural attributes and functional characteristics that specifically identify members of the genus defined by the claims, discloses a correlation between the asserted functions and structures, and describes assays for identifying sequences having the asserted functions, one of ordinary skill would undoubtedly have understood that Applicants described the nucleic acids defined by claims 3, 8, and 14-18 at the time of filing. The written description requirement is clearly met because the original disclosure provided sufficient information to show that the inventors possessed the invention at the time of filing, and persons of ordinary skill in the art would have recognized that Applicants invented what is claimed.

For at least these reasons, Applicants respectfully submit that the rejection is improper and request that it be withdrawn.

Rejections Under 35 USC § 112, Second Paragraph.

Claims 3, 10-11, 21-24, 26-28, 30-36, 44-48, 62-66, 74-79, 93-94, 105, and 111 were rejected under 35 USC § 112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter with Applicant regards as his invention. The rejection of claims 24, 30, 32, 34, 45, 105, and 111 has been mooted by their cancellation. The rejection of the remaining claims is traversed in part and overcome in part as discussed below.

Claims 3 and 111 were rejected as vague and indefinite due to inadvertent incorrect dependencies. Office Action, page 5. The rejection of claim 3 has been overcome by amending claim 3 to be dependent on claim 1. The rejection of claim 111 has been mooted by its cancellation.

Additionally, claims 10, 21-24, 26-28, and 30-36 were rejected as allegedly vague and indefinite because each recites "a limitation where the claimed nucleic acid comprises residues, substitutions or deletions 'corresponding to about' specific residues of the consensus sequence shown in Figure 8 (i.e., SEQ ID NO:21)." *Id.* at page 6. The Examiner finds that "[t]hese limitations are vague and indefinite in that it is unclear how many residues are encompassed by the term 'corresponding to about.' Does this term specify +/- three nucleotide residues? Ten nucleotide residues or a hundred residues?" *Id.* As noted above, the rejection of claims 24, 30, 32, and 34 has been mooted by the cancellation of those claims. Applicants respectfully note that claims 26 and 33 do not contain the phrase "corresponding to about." Claims 10, 21-23, 27-28, 31, 35, and 36 have been amended to delete the term "about" in the recited phrase, thereby overcoming this rejection.

The Examiner also suggested that the claims be amended to specifically recite SEQ ID NO:21, since this is the consensus sequence shown in Figures 8A-8I. Claims 10, 21, 26, 27, 31, and 35 have been amended as suggested.

Claim 36 was rejected as being allegedly vague and indefinite in that the metes and bounds of the claim are unclear. The Examiner states that "it is unclear how a nucleic acid can have a deletion of approximately 193 nucleotides from within the middle of SEQ ID NO:8 and retain the required 98% identity to SEQ ID NO:8 (i.e. a change of ~190 nucleotides out of a total of 1,767 nucleotides is ~10% difference)." Office Action, page 6, 2nd para. This rejection has been overcome by the amendments to claims 35 and 36. As amended, claim 35 specifies in part an isolated or recombinant nucleic acid comprising a polynucleotide sequence having at least 99% sequence identity to a nucleotide sequence which comprises the sequence of SEQ ID NO:8 with a deletion of one or more nucleotide residues in a region corresponding to nucleotide residue positions 319-512 of the consensus sequence shown in SEQ ID NO:21 (or the complementary sequence thereof). Support for this amendment is provided at, *e.g.*, original claims 1, 3, 7, and 35-37; page 11, lines 1-5; page 19, lines 15-16; and page 10, lines 9-11. The specification specifically provides for chimeric CMV promoter/enhancer homologue nucleic acids having at least 99.5% sequence identity to the sequence of SEQ ID NO:8 or fragments thereof. *See, e.g.*, page 11, lines 1-5. The specification describes fragments of SEQ ID NO:8 that lack one or more nucleotide residues in a region corresponding to

residue positions 319-512 of the consensus sequence shown in SEQ ID NO:21. *See, e.g.*, original claim 35. Thus, amended claim 35 now properly indicates nucleic acids having at least 99% identity to particular fragments of SEQ ID NO:8.

Amended claim 36 now properly specifies an isolated or recombinant nucleic acid comprising a polynucleotide sequence having at least 99% sequence identity to a nucleotide sequence which comprises the sequence of SEQ ID NO:8 with a deletion of nucleotide residues corresponding to residue positions 319-512 of the consensus sequence shown in SEQ ID NO:21 (or the complement thereof), wherein the polynucleotide sequence promotes expression of a nucleic acid encoding a polypeptide to which the polynucleotide sequence is operably linked. A deletion of residues 319-512 from SEQ ID NO:8 is a deletion of 194 residues (*i.e.*, 193+1=194). Thus, this particular fragment of SEQ ID NO:8 is 1573 nucleotides in length (*i.e.*, 1767-194=1573). A change of 1% of the nucleotides out of a total of 1573 nucleotides represents a change of 15 or 16 nucleotides.

With these amendments, Applicants believe the rejection of these claims has been overcome. Withdrawal of the rejection is respectfully requested.

To ensure clarity, claim 27 has been similarly amended to recite more particularly an isolated or recombinant nucleic acid comprising a polynucleotide sequence having at least 99% sequence identity to a nucleotide sequence which comprises the sequence of SEQ ID NO:8 with a deletion of one or more nucleotide residues in a region corresponding to residue positions 684-735 of the consensus sequence shown in SEQ ID NO:21 (or to a complementary sequence thereof). Support for this amendment is provided at, *e.g.*, original claims 1, 3, 7, 27-28, 37; page 10, lines 9-11; page 11, lines 1-5; and page 19, lines 15-16. Claim 28 has been amended to specify that the isolated or recombinant nucleic acid of claim 27 comprises a polynucleotide sequence having at least 99% sequence identity to a nucleotide sequence which comprises the sequence of SEQ ID NO:8 with a deletion of nucleotide residues corresponding to nucleotide residue positions 684-735 of the consensus sequence. Support for this amendments is provided at, *e.g.*, original claims 1, 3, 7, 27-28, 37; page 10, lines 9-11; page 11, lines 1-5; and page 19, lines 15-16. A deletion of residues 684-735 from SEQ ID NO:8 is a deletion of 52 residues (*i.e.*, 51+1=52). Thus, this particular fragment of SEQ ID NO:8 is 1715 nucleotides in length (*i.e.*, 1767-52=1715). A change of 1% of the nucleotides out of a total of 1715 nucleotides represents a change of 17 or 18 nucleotides.

Rejections Under 35 USC § 102.

1. Chapman

Claims 1, 3, 12, 14-18, 24, 26-28, 35-36, 44-48, 62-66, 74-78, 105, and 107 were rejected under 35 USC § 102(b) as allegedly being anticipated by Chapman *et al.*, *Nucl. Acids Res.* 19(14):3979-3986 (1991) [hereinafter "Chapman"]. The Examiner finds that Chapman discloses an hCMV sequence that has only 95.8% sequence identity over the entire length of the polynucleotide sequence of SEQ ID NO:8, but discloses an arbitrary subsequence that has a local similarity to SEQ ID NO:8 of 98.8% over residues 335-2099 of the 2.4 kb sequence of hCMV. Office Action, page 7, 1st and 2nd paras.

The Examiner finds that Applicants' amendments to the claims to delete the term "at least about 99%" sequence identity has obviated certain grounds of rejection for those embodiments that now read "at least 99%" sequence identity to SEQ ID NO:8. *Id.*, page 9, 1st para. However, the Examiner maintains the rejection for some claims (*e.g.*, claim 3). The Examiner is of the view that the term "about equal to" in the limitation "at a level that is about equal to or greater than" in certain claims "can be interpreted broadly to encompass a broad range of promoter activities." *Id.* at page 9, 2nd para. The Examiner takes the position that "the degree of sequence similarity between the Chapman et al. sequence and SEQ ID NO:8 is such that one of skill in the art would necessarily expect that the Chapman sequence would at least retain some promoter activity, which would be sufficient to meet the broad limitation of being 'at a level of about equal to' that of the reference promoters." *Id.* The Examiner also finds that "the term 'corresponding to about' as applied to residues of the consensus sequence is not explicitly defined in the specification, such that the term can be interpreted to read broadly on any number of residues." *Id.* at page 10, 1st full para.

This rejection is traversed in part and overcome in part as follows.

The rejection of claims 12, 24, 45, and 105 has been mooted by their cancellation. With regard to the remaining rejected claims, Applicants continue to traverse the anticipation rejection with regard to Chapman for at least the reasons stated in the Amendment filed on December 1, 2003. As discussed therein, Chapman does not teach the isolated or recombinant nucleic acid as particularly defined by claim 1. Moreover, as discussed therein, Chapman does not teach each of the additional specific limitations included in any claim dependent thereon.

However, to expedite prosecution of the instant application, claim 1 has been amended to specify more particularly an isolated or recombinant nucleic acid comprising a

polynucleotide sequence that has at least 99% sequence identity *to the entire length of the polynucleotide sequence of SEQ ID NO:8.* Claim 7 has been amended to specify that the nucleic acid of claim 1 comprises a polynucleotide sequence that has at least 99.5% sequence identity to the sequence of SEQ ID NO:8 or the complementary polynucleotide sequence thereof. *See, e.g.*, the specification at page 11, lines 1-5. Claim 8 has been amended to depend from claim 7.

With this amendment, Applicants believe the rejection of claim 1 (and pending claims 3, 14-18, 26, 44, 46-48, 62-66, and 74-78 ultimately dependent thereon) has been overcome. Chapman does not disclose any isolated or recombinant nucleic acid comprising a polynucleotide sequence that has at least 99% sequence identity to the entire length of the polynucleotide sequence of SEQ ID NO:8 (or the complementary polynucleotide sequence thereof) and that promotes expression of a polypeptide-encoding nucleic acid to which it is operably linked.

As discussed above, amended claim 27 properly specifies a nucleic acid comprising a polynucleotide sequence having at least 99% identity to a nucleotide sequence which comprises the sequence of SEQ ID NO:8 with a deletion of one or more nucleotide residues in a region corresponding to residue positions 684-735 of the consensus sequence shown in SEQ ID NO:2, or to a complementary sequence thereof. For example, a fragment of SEQ ID NO:8 in which one residue has been deleted has a length of 1766 nucleotides. A change of 1% of the nucleotides out of a total of 1766 nucleotides represents a change of 17 or 18 nucleotides. Similarly, a fragment of SEQ ID NO:8 that lacks all nucleotide residues at positions 684-735 (i.e., 52 residues) has a length of 1715 nucleotides (*i.e.*, 1767-52=1715), and a change of 1% of the nucleotides out of a total of 1715 nucleotides represents a change of 17 or 18 nucleotides. Amended claim 28 properly specifies a nucleic acid comprising a polynucleotide sequence having at least 99% identity to a nucleotide sequence which comprises a particular fragment of SEQ ID NO:8. This fragment lacks residues 684-735 (*i.e.*, 52 residues) of SEQ ID NO:8 and thus is 1715 nucleotides in length. A change of 1% of the nucleotides out of a total of 1715 nucleotides represents a change of 17 or 18 nucleotides. With these amendments, the rejection of claims 27 and 28 is overcome, since Chapman does not disclose the nucleic acids defined by these claims.

Amended claim 35 properly recites a nucleic acid comprising a polynucleotide sequence having at least 99% identity to a nucleotide sequence which comprises the sequence of SEQ ID NO:8 with a deletion of one or more nucleotide residues in a region corresponding to residue positions 319-512 of the consensus sequence shown in SEQ ID NO:21 (or the

complementary sequence thereof). Amended claim 36 specifies a polynucleotide sequence having at least 99% identity to a nucleotide sequence comprising the sequence of SEQ ID NO:8 with a deletion of nucleotide residues corresponding to residue positions 319-512 of the consensus sequence. As discussed above, this particular fragment is 1573 nucleotides in length. The rejection of claims 35 and 36 is overcome, because Chapman does not disclose the nucleic acids defined by these claims.

Claims 3 and 8 have been amended to delete the term "about" in the phrase "at a level of about equal to" and claims 10, 21, 22, 23, 27, 28, 31, 35, and 36 have been amended to delete the term "about" in the phrase "corresponding to about" in reference to particular residues of the consensus sequence. With these amendments, Applicants believe the Examiner's concerns regarding these phrases are alleviated.

For at least these reasons, Applicants respectfully submit that the rejection has been overcome and request that it be withdrawn.

2. U.S. Patent No. 6,200,959 to Haynes

Claims 1, 3, 7-8, 12, 14-18, 44-48, 62-66, 74-79, 93-94, 106-108, and 111-119 were rejected under 35 USC § 102(b) as allegedly being anticipated by Haynes *et al.* (U.S. Patent No. 6,200,959) [hereinafter "the '959 patent"]. Office Action at page 10, 2nd para. The Examiner finds that the '959 patent discloses "the construction and use of WRG7077, a 4,326 bp expression vector, for expressing a sequence encoding a viral antigen. *Id.* at page 10, 3rd para. The Examiner finds that the '959 patent teaches that this "vector comprises an HCMV IE promoter operatively linked to a multiple cloning site for insertion of antigen coding sequences." *Id.* The Examiner further finds that the promoter sequence from pWRG7077 disclosed by Haynes has 99.1% sequence across nucleotides 123-1765 of SEQ ID NO:8. *Id.* at pages 10-11, bridging para. The Examiner is of the view that given the high degree of identity between the sequence taught by the '959 patent and SEQ ID NO:8, Applicants' own data showing enhanced activity for SEQ ID NO:8, and given the fact that the Haynes *et al.* demonstrate sufficient promoter activity for SEQ ID NO:7 of their invention to generate an immune response in test animals, it is reasonable to expect that the promoters taught by Haynes *et al.* would have greater and/or different levels of promoter activity than the reference promoters described by SEQ ID NOS:19 and 20. *Id.* at page 11, 1st full para. The Examiner also finds that the term "about equal to" is not explicitly defined in the specification with regard top

relative levels of gene expression and can be interpreted broadly to encompass a broad range of promoter activities. *Id.* Based on these findings, the Examiner concludes that "[t]he degree of sequence similarity between the '959 sequence and SEQ ID NO:8 is such that one of skill in the art would necessarily expect that the '959 sequence would at least retain some promoter activity, which would be sufficient to meet the broad limitation of being 'at a level of about equal' to that of the reference promoters." *Id.*

The rejection of claims 45, 108, 111-112, and 117 has been mooted by their cancellation. The rejection of the remaining claims is traversed in part and overcome in part as follows.

Applicants respectfully traverse the Examiner's assertion that it is reasonable to expect that the sequence described in the '959 patent would have greater or different levels of promoter activity that the human CMV promoter represented by either SEQ ID NO:19 and 20 or that the '959 patent sequence would have an ability to promote expression of an operably linked polypeptide-encoding sequence that is approximately equal to that of either SEQ ID NO:19 or 20. Nevertheless, to expedite prosecution, claims 1, 106, and 113 have been amended to specify more particularly a nucleic acid comprising a polynucleotide sequence that has at least 99% sequence identity to the *entire length of the polynucleotide sequence of SEQ ID NO:8* and promotes expression of a nucleic acid encoding a polypeptide to which it is operably linked. The '959 patent does not disclose any polynucleotide sequence having at least 99% sequence identity over the entire length of the sequence of SEQ ID NO:8. Nor does the '959 patent disclose any such sequence which also has the functional limitations required by these claims.

Claim 7 has been amended to recite more specifically that the nucleic acid of claim 1 comprises a polynucleotide sequence that has at least 99.5% sequence identity to the polynucleotide sequence of SEQ ID NO:8 or the complementary polynucleotide sequence thereof. As recognized by the Examiner, the '959 patent does not disclose such a nucleic acid.

For at least these reasons, the rejection of claims 1, 106, and 133, and all claims dependent thereon, has been overcome. Withdrawal of the rejection is respectfully requested.

Rejections Under 35 USC § 101.

Claims 65-66 and 118-119 were rejected under 35 USC § 101 because the claimed invention can be interpreted as reading on human being (i.e. non-statutory subject matter). This

rejection has been overcome by amending these claims to specify an "isolated or recombinant" cell. Withdrawal of the rejection is respectfully requested.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested. If a telephone conference would expedite prosecution of this application in any way, the Examiner is invited to telephone the undersigned at (650) 298-5809.

Respectfully submitted,

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